

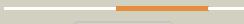
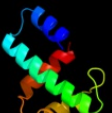




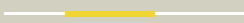





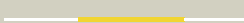
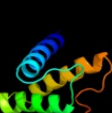

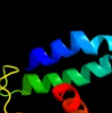

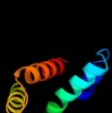


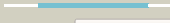

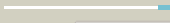


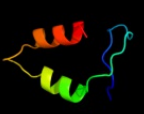





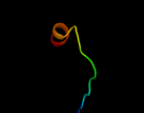







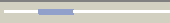


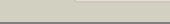





#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1a0pa1	 Alignment		92.5	23	Fold: SAM domain-like Superfamily: lambda integrase-like, N-terminal domain Family: lambda integrase-like, N-terminal domain
2	c1a0pA	 Alignment		89.3	24	PDB header: dna recombination Chain: A: PDB Molecule: site-specific recombinase xerd; PDBTitle: site-specific recombinase, xerd
3	c1crxA	 Alignment		84.9	12	PDB header: replication/dna Chain: A: PDB Molecule: cre recombinase; PDBTitle: cre recombinase/dna complex reaction intermediate i
4	c3lysC	 Alignment		79.2	19	PDB header: recombination Chain: C: PDB Molecule: prophage pi2 protein 01, integrase; PDBTitle: crystal structure of the n-terminal domain of the prophage2 pi2 protein 01 (integrase) from lactococcus lactis,3 northeast structural genomics consortium target kr124f
5	c2keyA	 Alignment		77.7	6	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: putative phage integrase; PDBTitle: solution nmr structure of a domain from a putative phage integrase2 protein bf2284 from bacteroides fragilis, northeast structural3 genomics consortium target bfr257c
6	c1ma7A	 Alignment		77.4	11	PDB header: hydrolase, ligase/dna Chain: A: PDB Molecule: cre recombinase; PDBTitle: crystal structure of cre site-specific recombinase2 complexed with a mutant dna substrate, loxp-a8/t27
7	c2oxoA	 Alignment		73.5	12	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: crystallization and structure determination of the core-2 binding domain of bacteriophage lambda integrase
8	d1f44a1	 Alignment		72.1	14	Fold: SAM domain-like Superfamily: lambda integrase-like, N-terminal domain Family: lambda integrase-like, N-terminal domain
9	c2khqA	 Alignment		71.0	14	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: solution nmr structure of a phage integrase ssp19472 fragment 59-159 from staphylococcus saprophyticus,3 northeast structural genomics consortium target syr103b
10	c3nrwA	 Alignment		63.9	15	PDB header: recombination Chain: A: PDB Molecule: phage integrase/site-specific recombinase; PDBTitle: crystal structure of the n-terminal domain of phage integrase/site-2 specific recombinase (tnp) from haloarcula marismortui, northeast3 structural genomics consortium target hmr208a
11	c3axtA	 Alignment		46.7	17	PDB header: transferase Chain: A: PDB Molecule: probable n(2),n(2)-dimethylguanosine trna methyltransferase PDBTitle: complex structure of trna methyltransferase trm1 from aquifex aeolicus2 with s-adenosyl-l-methionine

12	d2dula1	 Alignment		39.9	10	Fold: S-adenosyl-L-methionine-dependent methyltransferases Superfamily: S-adenosyl-L-methionine-dependent methyltransferases Family: TRM1-like
13	c2kkaA	 Alignment		39.1	20	PDB header: dna binding protein Chain: A: PDB Molecule: phage integrase; PDBTitle: solution nmr structure of the phage integrase sam-like2 domain from moth 1796 from moorella thermoacetica.3 northeast structural genomics consortium target mtr39k4 (residues 64-171).
14	d1m4za	 Alignment		38.9	20	Fold: SH3-like barrel Superfamily: BAH domain Family: BAH domain
15	c2fvuA	 Alignment		34.3	28	PDB header: transcription Chain: A: PDB Molecule: regulatory protein sir3; PDBTitle: structure of the yeast sir3 bah domain
16	c2kiwA	 Alignment		31.4	5	PDB header: dna binding protein Chain: A: PDB Molecule: int protein; PDBTitle: solution nmr structure of the domain n-terminal to the2 integrase domain of sh1003 from staphylococcus3 haemolyticus. northeast structural genomics consortium4 target shr105f (64-166).
17	d1jga2	 Alignment		30.3	32	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
18	c2kkaA	 Alignment		29.9	14	PDB header: dna binding protein Chain: A: PDB Molecule: integrase; PDBTitle: solution nmr structure of an integrase domain from protein2 spa4288 from salmonella enterica, northeast structural3 genomics consortium target slr105h
19	c1pbyA	 Alignment		28.6	24	PDB header: oxidoreductase Chain: A: PDB Molecule: quinoxemoprotein amine dehydrogenase 60 kda PDBTitle: structure of the phenylhydrazine adduct of the2 quinoxemoprotein amine dehydrogenase from paracoccus3 denitrificans at 1.7 a resolution
20	c1jmxA	 Alignment		25.0	24	PDB header: oxidoreductase Chain: A: PDB Molecule: amine dehydrogenase; PDBTitle: crystal structure of a quinoxemoprotein amine dehydrogenase2 from pseudomonas putida
21	d1k3ka	 Alignment	not modelled	24.6	17	Fold: Toxins' membrane translocation domains Superfamily: Bcl-2 inhibitors of programmed cell death Family: Bcl-2 inhibitors of programmed cell death
22	d2cora1	 Alignment	not modelled	23.3	30	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
23	d2dara1	 Alignment	not modelled	21.5	40	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
24	c1m1zB	 Alignment	not modelled	21.3	30	PDB header: hydrolase Chain: B: PDB Molecule: beta-lactam synthetase; PDBTitle: beta-lactam synthetase apo enzyme
25	c2kd1A	 Alignment	not modelled	19.6	9	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: dna integration/recombination/inversion protein; PDBTitle: solution nmr structure of the integrase-like domain from2 bacillus cereus ordered locus bc_1272. northeast3 structural genomics consortium target bcr268f
26	d2c9wa1	 Alignment	not modelled	17.3	44	Fold: SOCS box-like Superfamily: SOCS box-like Family: SOCS box-like
27	c2p7vA	 Alignment	not modelled	16.6	15	PDB header: transcription Chain: A: PDB Molecule: regulator of sigma d; PDBTitle: crystal structure of the escherichia coli regulator of sigma 70, rsd,2 in complex with sigma 70 domain 4
28	d2cta1a	 Alignment	not modelled	13.2	31	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2

29	c1x6aA	Alignment	not modelled	13.0	18	PDB header: protein binding Chain: A: PDB Molecule: lim domain kinase 2; PDBTitle: solution structures of the second lim domain of human lim-2 kinase 2 (limk2)
30	c1l6nA	Alignment	not modelled	12.4	18	PDB header: viral protein Chain: A: PDB Molecule: gag polyprotein; PDBTitle: structure of the n-terminal 283-residue fragment of the hiv-2 1 gag polyprotein
31	c2l76A	Alignment	not modelled	11.7	15	PDB header: transcription Chain: A: PDB Molecule: nfatc2-interacting protein; PDBTitle: solution nmr structure of human nfatc2ip ubiquitin-like domain,2 nfatc2ip_244_338, nesg target ht65a/ocsp target hs00387_244_338/sgc-3 toronto
32	c2a3vA	Alignment	not modelled	11.6	14	PDB header: recombination Chain: A: PDB Molecule: site-specific recombinase int4; PDBTitle: structural basis for broad dna-specificity in integron2 recombination
33	d2fk4a1	Alignment	not modelled	11.4	22	Fold: E6 C-terminal domain-like Superfamily: E6 C-terminal domain-like Family: E6 C-terminal domain-like
34	d1p7da	Alignment	not modelled	11.2	8	Fold: DNA breaking-rejoining enzymes Superfamily: DNA breaking-rejoining enzymes Family: Lambda integrase-like, catalytic core
35	d2cta2	Alignment	not modelled	10.7	63	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
36	c2corA	Alignment	not modelled	10.7	30	PDB header: structural protein Chain: A: PDB Molecule: pinch protein; PDBTitle: solution structure of the third lim domain of particularly2 interesting new cys-his protein
37	d1b8ta4	Alignment	not modelled	10.4	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
38	d2yt9a1	Alignment	not modelled	9.9	33	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
39	d1ct9a2	Alignment	not modelled	9.2	22	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
40	c2dj7A	Alignment	not modelled	9.1	25	PDB header: metal binding protein Chain: A: PDB Molecule: actin-binding lim protein 3; PDBTitle: solution structure of 3rd lim domain of actin-binding lim2 protein 3
41	d1ubdc2	Alignment	not modelled	8.8	50	Fold: beta-beta-alpha zinc fingers Superfamily: beta-beta-alpha zinc fingers Family: Classic zinc finger, C2H2
42	c1ct9D	Alignment	not modelled	8.7	22	PDB header: ligase Chain: D: PDB Molecule: asparagine synthetase b; PDBTitle: crystal structure of asparagine synthetase b from2 escherichia coli
43	c2jhdA	Alignment	not modelled	8.6	26	PDB header: cell adhesion Chain: A: PDB Molecule: micronemal protein 1; PDBTitle: crystal structure of toxoplasma gondii micronemal protein 12 bound to 3'-sialyl-n-acetyl-lactosamine
44	c3h3pT	Alignment	not modelled	8.6	46	PDB header: immune system Chain: T: PDB Molecule: 4e10_s0_1tjlc_004_n; PDBTitle: crystal structure of hiv epitope-scaffold 4e10 fv complex
45	c1x31D	Alignment	not modelled	8.5	13	PDB header: oxidoreductase Chain: D: PDB Molecule: sarcosine oxidase delta subunit; PDBTitle: crystal structure of heterotetrameric sarcosine oxidase from2 corynebacterium sp. u-96
46	d1vqqq1	Alignment	not modelled	8.4	23	Fold: SH3-like barrel Superfamily: Translation proteins SH3-like domain Family: Ribosomal proteins L24p and L21e
47	d1k5oa	Alignment	not modelled	8.2	14	Fold: Myosin phosphatase inhibitor 17kDa protein, CPI-17 Superfamily: Myosin phosphatase inhibitor 17kDa protein, CPI-17 Family: Myosin phosphatase inhibitor 17kDa protein, CPI-17
48	c3rxyA	Alignment	not modelled	8.1	13	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: nif3 protein; PDBTitle: crystal structure of nif3 superfamily protein from sphaerobacter2 thermophilus
49	c3dr0B	Alignment	not modelled	8.1	38	PDB header: electron transport Chain: B: PDB Molecule: cytochrome c6; PDBTitle: structure of reduced cytochrome c6 from synechococcus sp.2 pcc 7002
50	d1wh7a	Alignment	not modelled	7.9	14	Fold: DNA/RNA-binding 3-helical bundle Superfamily: Homeodomain-like Family: Homeodomain
51	d2dasa1	Alignment	not modelled	7.9	50	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: TRASH domain
52	c2zkrq	Alignment	not modelled	7.7	29	PDB header: ribosomal protein/rna Chain: Q: PDB Molecule: rna expansion segment es31 part ii; PDBTitle: structure of a mammalian ribosomal 60s subunit within an2 80s complex obtained by docking homology models of the rna3 and proteins into an 8.7 a cryo-em map
53	c1x4uA	Alignment	not modelled	7.6	31	PDB header: lipid binding protein Chain: A: PDB Molecule: zinc finger, fyve domain containing 27 isoform b; PDBTitle: solution structure of the fyve domain from human fyve2 domain containing 27 isoform b protein
54	d1chma1	Alignment	not modelled	7.5	42	Fold: Ribonuclease H-like motif Superfamily: Creatinase/prolidase N-terminal domain Family: Creatinase/prolidase N-terminal domain

55	c3q8dB	Alignment	not modelled	7.3	45	PDB header: dna binding protein Chain: B: PDB Molecule: dna repair protein reco; PDBTitle: e. coli reco complex with ssb c-terminus
56	d2izva1	Alignment	not modelled	7.2	33	Fold: SOCS box-like Superfamily: SOCS box-like Family: SOCS box-like
57	d1b8ta2	Alignment	not modelled	7.1	43	Fold: Glucocorticoid receptor-like (DNA-binding domain) Superfamily: Glucocorticoid receptor-like (DNA-binding domain) Family: LIM domain
58	c2zonG	Alignment	not modelled	7.1	25	PDB header: oxidoreductase/electron transport Chain: G: PDB Molecule: cytochrome c551; PDBTitle: crystal structure of electron transfer complex of nitrite2 reductase with cytochrome c
59	c2l4dA	Alignment	not modelled	7.0	38	PDB header: electron transport Chain: A: PDB Molecule: sco1/senc family protein/cytochrome c; PDBTitle: cytochrome c domain of pp3183 protein from pseudomonas putida
60	c2zshB	Alignment	not modelled	6.9	6	PDB header: hormone receptor Chain: B: PDB Molecule: della protein gai; PDBTitle: structural basis of gibberellin(ga3)-induced della2 recognition by the gibberellin receptor
61	d1kv9a1	Alignment	not modelled	6.9	25	Fold: Cytochrome c Superfamily: Cytochrome c Family: Quinoprotein alcohol dehydrogenase, C-terminal domain
62	c3cu4A	Alignment	not modelled	6.8	63	PDB header: electron transport Chain: A: PDB Molecule: cytochrome c family protein; PDBTitle: omcf, outer membrane cytochrome f from geobacter2 sulfurreducers
63	d2gc4d1	Alignment	not modelled	6.8	25	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
64	d1cyja	Alignment	not modelled	6.8	38	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
65	c2dasA	Alignment	not modelled	6.8	50	PDB header: metal transport Chain: A: PDB Molecule: zinc finger mym-type protein 5; PDBTitle: solution structure of trash domain of zinc finger mym-type2 protein 5
66	d1wfpa	Alignment	not modelled	6.7	55	Fold: AN1-like Zinc finger Superfamily: AN1-like Zinc finger Family: AN1-like Zinc finger
67	c1s6wA	Alignment	not modelled	6.6	80	PDB header: antibiotic Chain: A: PDB Molecule: hepcidin; PDBTitle: solution structure of hybrid white striped bass hepcidin
68	d1dy7b1	Alignment	not modelled	6.5	38	Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
69	d1h9xa1	Alignment	not modelled	6.5	38	Fold: Cytochrome c Superfamily: Cytochrome c Family: N-terminal (heme c) domain of cytochrome cd1-nitrite reductase
70	c2cuqA	Alignment	not modelled	6.5	21	PDB header: structural genomics, unknown function Chain: A: PDB Molecule: four and a half lim domains 3; PDBTitle: solution structure of second lim domain from human skeletal2 muscle lim-protein 2
71	c1q15A	Alignment	not modelled	6.5	25	PDB header: biosynthetic protein Chain: A: PDB Molecule: cara; PDBTitle: carbapenam synthetase
72	d1q15a2	Alignment	not modelled	6.5	14	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
73	c2v07A	Alignment	not modelled	6.5	25	PDB header: photosynthesis Chain: A: PDB Molecule: cytochrome c6; PDBTitle: structure of the arabidopsis thaliana cytochrome c6a v52q2 variant
74	c3rf1B	Alignment	not modelled	6.3	30	PDB header: ligase Chain: B: PDB Molecule: glycyl-trna synthetase alpha subunit; PDBTitle: the crystal structure of glycyl-trna synthetase subunit alpha from2 campylobacter jejuni subsp. jejuni nctc 11168
75	c2eluA	Alignment	not modelled	6.3	36	PDB header: transcription Chain: A: PDB Molecule: zinc finger protein 406; PDBTitle: solution structure of the 5th c2h2 zinc finger of human2 zinc finger protein 406
76	d1sqna	Alignment	not modelled	6.1	12	Fold: Nuclear receptor ligand-binding domain Superfamily: Nuclear receptor ligand-binding domain Family: Nuclear receptor ligand-binding domain
77	d2c8sa1	Alignment	not modelled	6.1	38	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
78	d2a1ja1	Alignment	not modelled	6.1	14	Fold: SAM domain-like Superfamily: RuvA domain 2-like Family: Hef domain-like
79	d1j3sa	Alignment	not modelled	6.0	20	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
80	c2cqjA	Alignment	not modelled	6.0	31	PDB header: rna binding protein Chain: A: PDB Molecule: u3 small nucleolar ribonucleoprotein protein PDBTitle: solution structure of the s4 domain of u3 small nucleolar2 ribonucleoprotein protein imp3 homolog
						Fold: AN1-like Zinc finger

81	d1wffa_	Alignment	not modelled	6.0	45	Superfamily: AN1-like Zinc finger Family: AN1-like Zinc finger
82	d1xffa_	Alignment	not modelled	5.9	25	Fold: Ntn hydrolase-like Superfamily: N-terminal nucleophile aminohydrolases (Ntn hydrolases) Family: Class II glutamine amidotransferases
83	c3h5gB_	Alignment	not modelled	5.8	45	PDB header: de novo protein Chain: B: PDB Molecule: coil ser l16d-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
84	c3h5fB_	Alignment	not modelled	5.8	45	PDB header: de novo protein Chain: B: PDB Molecule: coil ser l16l-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
85	c3h5gC_	Alignment	not modelled	5.8	45	PDB header: de novo protein Chain: C: PDB Molecule: coil ser l16d-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
86	c3h5gA_	Alignment	not modelled	5.8	45	PDB header: de novo protein Chain: A: PDB Molecule: coil ser l16d-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
87	c3h5fA_	Alignment	not modelled	5.8	45	PDB header: de novo protein Chain: A: PDB Molecule: coil ser l16l-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
88	c3h5fC_	Alignment	not modelled	5.8	45	PDB header: de novo protein Chain: C: PDB Molecule: coil ser l16l-pen; PDBTitle: switching the chirality of the metal environment alters the2 coordination mode in designed peptides.
89	c3k35D_	Alignment	not modelled	5.8	21	PDB header: hydrolase Chain: D: PDB Molecule: nad-dependent deacetylase sirtuin-6; PDBTitle: crystal structure of human sirt6
90	d1cc5a_	Alignment	not modelled	5.8	25	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
91	c2x6pA_	Alignment	not modelled	5.7	45	PDB header: de novo protein Chain: A: PDB Molecule: coil ser l19c; PDBTitle: crystal structure of coil ser l19c
92	c2x6pB_	Alignment	not modelled	5.7	45	PDB header: de novo protein Chain: B: PDB Molecule: coil ser l19c; PDBTitle: crystal structure of coil ser l19c
93	c2x6pC_	Alignment	not modelled	5.7	45	PDB header: de novo protein Chain: C: PDB Molecule: coil ser l19c; PDBTitle: crystal structure of coil ser l19c
94	d1j2na_	Alignment	not modelled	5.7	14	Fold: Myosin phosphatase inhibitor 17kDa protein, CPI-17 Superfamily: Myosin phosphatase inhibitor 17kDa protein, CPI-17 Family: Myosin phosphatase inhibitor 17kDa protein, CPI-17
95	d1c6ra_	Alignment	not modelled	5.7	38	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
96	c1jxaA_	Alignment	not modelled	5.6	24	PDB header: transferase Chain: A: PDB Molecule: glucosamine 6-phosphate synthase; PDBTitle: glucosamine 6-phosphate synthase with glucose 6-phosphate
97	d1c6sa_	Alignment	not modelled	5.6	38	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
98	d1f1fa_	Alignment	not modelled	5.6	38	Fold: Cytochrome c Superfamily: Cytochrome c Family: monodomain cytochrome c
99	c1x4lA_	Alignment	not modelled	5.4	30	PDB header: metal binding protein Chain: A: PDB Molecule: skeletal muscle lim-protein 3; PDBTitle: solution structure of lim domain in four and a half lim2 domains protein 2